

seqlist.txt

SEQUENCE LISTING

<110> Novartis AG
Wolfgang, Curt

<120> BIOMARKERS FOR THE PREDICTION OF
DRUG-INDUCED DIARRHOEA

<130> ON/4-33391A

<150> 60/508,973

<151> 2003-10-06

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2187

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (104)...(1618)

<223> Human interferon regulatory factor 5 (IRF5) mRNA
coding region

<400> 1

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                               Met Asn Gln Ser
                               1

atc cca gtg gct ccc acc cca ccc cgc cgc gtg cgg ctg aag ccc tgg 163
Ile Pro Val Ala Pro Thr Pro Pro Arg Arg Val Arg Leu Lys Pro Trp
 5                               10                               15                               20

ctg gtg gcc cag gtg aac agc tgc cag tac cca ggg ctt caa tgg gtc 211
Leu Val Ala Gln Val Asn Ser Cys Gln Tyr Pro Gly Leu Gln Trp Val
                               25                               30                               35

aac ggg gaa aag aaa tta ttc tgc atc ccc tgg agg cat gcc aca agg 259
Asn Gly Glu Lys Lys Leu Phe Cys Ile Pro Trp Arg His Ala Thr Arg
                               40                               45                               50

cat ggt ccc agc cag gac gga gat aac acc atc ttc aag gcc tgg gcc 307
His Gly Pro Ser Gln Asp Gly Asp Asn Thr Ile Phe Lys Ala Trp Ala
                               55                               60                               65

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Lys Glu Thr Gly Lys Tyr Thr Glu Gly Val Asp Glu Ala Asp Pro Ala
                               70                               75                               80

aag tgg aag gcc aac ctg cgc tgt gcc ctt aac aag agc cgg gac ttc 403
Lys Trp Lys Ala Asn Leu Arg Cys Ala Leu Asn Lys Ser Arg Asp Phe
 85                               90                               95                               100

cgc ctc atc tac gac ggg ccc cgg gac atg cca cct cag ccc tac aag 451
Arg Leu Ile Tyr Asp Gly Pro Arg Asp Met Pro Pro Gln Pro Tyr Lys
                               105                               110                               115

atc tac gag gtc tgc tcc aat ggc cct gct ccc aca gac tcc cag ccc 499
Ile Tyr Glu Val Cys Ser Asn Gly Pro Ala Pro Thr Asp Ser Gln Pro
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seqlist.txt																
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gag Glu	ctg Leu 150	cag Gln	agg Arg	atg Met	ttg Leu	cca Pro 155	agc Ser	ctg Leu	agc Ser	ctc Leu	aca Thr 160	gat Asp	gca Ala	gtg Val	cag Gln	595
tct Ser 165	ggc Gly	ccc Pro	cac His	atg Met	aca Thr 170	ccc Pro	tat Tyr	tct Ser	tta Leu	ctc Leu 175	aaa Lys	gag Glu	gat Asp	gtc Val	aag Lys 180	643
tgg Trp	ccg Pro	ccc Pro	act Thr	ctg Leu 185	cag Gln	ccg Pro	ccc Pro	act Thr	ctg Leu 190	cag Gln	ccg Pro	ccc Pro	gtg Val	gtg Val 195	ctg Leu	691
ggt Gly	ccc Pro	cct Pro	gct Ala 200	cca Pro	gac Asp	ccc Pro	agc Ser	ccc Pro 205	ctg Leu	gct Ala	cct Pro	ccc Pro	cct Pro 210	ggc Gly	aac Asn	739
cct Pro	gct Ala	ggc Gly 215	ttc Phe	agg Arg	gag Glu	ctt Leu	ctc Leu 220	tct Ser	gag Glu	gtc Val	ctg Leu	gag Glu 225	cct Pro	ggg Gly	ccc Pro	787
ctg Leu	cct Pro 230	gcc Ala	agc Ser	ctg Leu	ccc Pro	cct Pro 235	gca Ala	ggc Gly	gaa Glu	cag Gln	ctc Leu 240	ctg Leu	cca Pro	gac Asp	ctg Leu	835
ctg Leu 245	atc Ile	agc Ser	ccc Pro	cac His	atg Met 250	ctg Leu	cct Pro	ctg Leu	acc Thr	gac Asp 255	ctg Leu	gag Glu	atc Ile	aag Lys	ttt Phe 260	883
cag Gln	tac Tyr	cgg Arg	ggg Gly	cgg Arg 265	cca Pro	ccc Pro	cgg Arg	gcc Ala	ctc Leu 270	acc Thr	atc Ile	agc Ser	aac Asn	ccc Pro 275	cat His	931
ggc Gly	tgc Cys	cgg Arg	ctc Leu 280	ttc Phe	tac Tyr	agc Ser	cag Gln	ctg Leu 285	gag Glu	gcc Ala	acc Thr	cag Gln	gag Glu 290	cag Gln	gtg Val	979
gaa Glu	ctc Leu	ttc Phe 295	ggc Gly	ccc Pro	ata Ile	agc Ser	ctg Leu 300	gag Glu	caa Gln	gtg Val	cgc Arg	ttc Phe 305	ccc Pro	agc Ser	cct Pro	1027
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gat Asp 325	gtc Val	ctg Leu	gac Asp	cgc Arg	ggg Gly 330	ctc Leu	atc Ile	ctc Leu	cag Gln	cta Leu 335	cag Gln	ggc Gly	cag Gln	gac Asp	ctt Leu 340	1123
tat Tyr	gcc Ala	atc Ile	cgc Arg	ctg Leu 345	tgt Cys	cag Gln	tgc Cys	aag Lys	gtg Val 350	ttc Phe	tgg Trp	agc Ser	ggg Gly	cct Pro 355	tgt Cys	1171
gcc Ala	tca Ser	gcc Ala	cat His 360	gac Asp	tca Ser	tgc Cys	ccc Pro	aac Asn 365	ccc Pro	atc Ile	cag Gln	cgg Arg	gag Glu 370	gtc Val	aag Lys	1219
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seq1ist.txt

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Phe Gly Glu Glu Trp Pro Asp Arg Lys Pro Arg Glu Lys Lys Leu Ile
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act gta cag gtg gtg cct gta gca gct cga ctg ctg ctg gag atg ttc 1411
Thr Val Gln Val Val Pro Val Ala Ala Arg Leu Leu Leu Glu Met Phe
425 430 435

tca ggg gag cta tct tgg tca gct gat agt atc cgg cta cag atc tca 1459
Ser Gly Glu Leu Ser Trp Ser Ala Asp Ser Ile Arg Leu Gln Ile Ser
440 445 450

aac cca gac ctc aaa gac cgc atg gtg gag caa ttc aag gag ctc cat 1507
Asn Pro Asp Leu Lys Asp Arg Met Val Glu Gln Phe Lys Glu Leu His
455 460 465

cac atc tgg cag tcc cag cag cgg ttg cag cct gtg gcc cag gcc cct 1555
His Ile Trp Gln Ser Gln Gln Arg Leu Gln Pro Val Ala Gln Ala Pro
470 475 480

cct gga gca ggc ctt ggt gtt ggc cag ggg ccc tgg cct atg cac cca 1603
Pro Gly Ala Gly Leu Gly Val Gly Gln Gly Pro Trp Pro Met His Pro
485 490 495 500

gct ggc atg caa taa caaggctgca gacggtgact ggccctggct tcctgggtgg 1658
Ala Gly Met Gln *
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cggtgcggac tgatgtggag atgtgacagc cccgatgagc acctggctgg ctgcagggtc 1718
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aggaattgcc taagggtggc ccactcttgt gattgccccca tttcctctgg caacaaaagc 1958
cagagtgttg tgggccaagt ccccccacag ggcctctgca gggcatggcc ctgatttccc 2018
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gtatcatatc agatgctcaa ggctggcagc taccctcttc ttgagagtcc aagaacctgg 2138
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<210> 2
<211> 1462
<212> DNA
<213> Homo sapiens
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<220>
<221> CDS
<222> (200)...(910)
<223> Human cell division cycle 34 (CDC34) mRNA coding
region
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<400> 2
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gcggcccggc ccgtctcgcg aactcgcggt ggtcgcgcgg ccccgcgctg ctccgacccc 180
gggcccctcc gccgccgcc atg gct cgg ccg cta gtg ccc agc tcg cag aag 232
Met Ala Arg Pro Leu Val Pro Ser Ser Gln Lys
1 5 10
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gcg ctg ctg ctg gag ctc aag ggg ctg cag gaa gag ccg gtc gag gga 280
Ala Leu Leu Leu Glu Leu Lys Gly Leu Gln Glu Glu Pro Val Glu Gly
15 20 25
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```

ttc cgc gtg aca ctg gtg gac gag ggc gat cta tac aac tgg gag gtg 328
Phe Arg Val Thr Leu Val Asp Glu Gly Asp Leu Tyr Asn Trp Glu Val
30 35 40
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```

gcc atc ttc ggg ccc ccc aac acc tac tac gag ggc ggc tac ttc aag 376
Ala Ile Phe Gly Pro Pro Asn Thr Tyr Tyr Glu Gly Gly Tyr Phe Lys
45 50 55
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seq1ist.txt

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gcg cgc ctc aag ttc ccc atc gac tac cca tac tct cca cca gcc ttt 424
Ala Arg Leu Lys Phe Pro Ile Asp Tyr Pro Tyr Ser Pro Pro Ala Phe
60 65 70 75

cgg ttc ctg acc aag atg tgg cac cct aac atc tac gag acg ggg gac 472
Arg Phe Leu Thr Lys Met Trp His Pro Asn Ile Tyr Glu Thr Gly Asp
80 85 90

gtg tgt atc tcc atc ctc cac ccg ccg gtg gac gac ccc cag agc ggg 520
Val Cys Ile Ser Ile Leu His Pro Pro Val Asp Asp Pro Gln Ser Gly
95 100 105

gag ctg ccc tca gag agg tgg aac ccc acg cag aac gtc agg acc att 568
Glu Leu Pro Ser Glu Arg Trp Asn Pro Thr Gln Asn Val Arg Thr Ile
110 115 120

ctc ctg agt gtg atc tcc ctc ctg aac gag ccc aac acc ttc tcg ccc 616
Leu Leu Ser Val Ile Ser Leu Leu Asn Glu Pro Asn Thr Phe Ser Pro
125 130 135

gca aac gtg gac gcc tcc gtg atg tac agg aag tgg aaa gag agc aag 664
Ala Asn Val Asp Ala Ser Val Met Tyr Arg Lys Trp Lys Glu Ser Lys
140 145 150 155

ggg aag gat cgg gag tac aca gac atc atc cgg aag cag gtc ctg ggg 712
Gly Lys Asp Arg Glu Tyr Thr Asp Ile Ile Arg Lys Gln Val Leu Gly
160 165 170

acc aag gtg gac gcg gag cgt gac ggc gtg aag gtg ccc acc acg ctg 760
Thr Lys Val Asp Ala Glu Arg Asp Gly Val Lys Val Pro Thr Thr Leu
175 180 185

gcc gag tac tgc gtg aag acc aag gcg ccg gcg ccc gac gag ggc tca 808
Ala Glu Tyr Cys Val Lys Thr Lys Ala Pro Ala Pro Asp Glu Gly Ser
190 195 200

gac ctc ttc tac gac gac tac tac gag gac ggc gag gtg gag gag gag 856
Asp Leu Phe Tyr Asp Asp Tyr Tyr Glu Asp Gly Glu Val Glu Glu Glu
205 210 215

gcc gac agc tgc ttc ggg gac gat gag gat gac tct ggc acg gag gag 904
Ala Asp Ser Cys Phe Gly Asp Asp Glu Asp Asp Ser Gly Thr Glu Glu
220 225 230 235

tcc tga caccaccaga ataaacttgc cgagttttacc tcactagggc cggacccgtg 960
Ser *

```

```

gctccttaga cgacagacta cctcacggag gttttgtgct ggtccccgtc tcctctgggt 1020
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<210> 3
 <211> 3505
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (125)...(784)
 <223> Human BCL2/adenovirus E1B 19kDa interacting

seqlist.txt
protein 3-like (BNIP3L) mRNA coding region

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tgtgttgctg cctgagtgcc ggagacggtc ctgctgctgc cgcagtcctg ccagctgtcc 120
gaca atg tgc tcc cac cta gtc gag ccg ccg ccg ccc ctg cac aac aac 169
Met Ser Ser His Leu Val Glu Pro Pro Pro Pro Leu His Asn Asn
1 5 10 15

aac aac aac tgc gag gaa aat gag cag tct ctg ccc ccg ccg gcc ggc 217
Asn Asn Asn Cys Glu Glu Asn Glu Gln Ser Leu Pro Pro Pro Ala Gly
20 25 30

ctc aac agt tcc tgg gtg gag cta ccc atg aac agc agc aat ggc aat 265
Leu Asn Ser Ser Trp Val Glu Leu Pro Met Asn Ser Ser Asn Gly Asn
35 40 45

gat aat ggc aat ggg aaa aat ggg ggg ctg gaa cac gta cca tcc tca 313
Asp Asn Gly Asn Gly Lys Asn Gly Gly Leu Glu His Val Pro Ser Ser
50 55 60

tcc tcc atc cac aat gga gac atg gag aag att ctt ttg gat gca caa 361
Ser Ser Ile His Asn Gly Asp Met Glu Lys Ile Leu Leu Asp Ala Gln
65 70 75

cat gaa tca gga cag agt agt tcc aga ggc agt tct cac tgt gac agc 409
His Glu Ser Gly Gln Ser Ser Ser Arg Gly Ser Ser His Cys Asp Ser
80 85 90 95

cct tcg cca caa gaa gat ggg cag atc atg ttt gat gtg gaa atg cac 457
Pro Ser Pro Gln Glu Asp Gly Gln Ile Met Phe Asp Val Glu Met His
100 105 110

acc agc agg gac cat agc tct cag tca gaa gaa gaa gtt gta gaa gga 505
Thr Ser Arg Asp His Ser Ser Gln Ser Glu Glu Glu Val Val Glu Gly
115 120 125

gag aag gaa gtc gag gct ttg aag aaa agt gcg gac tgg gta tca gac 553
Glu Lys Glu Val Glu Ala Leu Lys Lys Ser Ala Asp Trp Val Ser Asp
130 135 140

tgg tcc agt aga ccc gaa aac att cca ccc aag gag ttc cac ttc aga 601
Trp Ser Ser Arg Pro Glu Asn Ile Pro Pro Lys Glu Phe His Phe Arg
145 150 155

cac cct aaa cgt tct gtg tct tta agc atg agg aaa agt gga gcc atg 649
His Pro Lys Arg Ser Val Ser Leu Ser Met Arg Lys Ser Gly Ala Met
160 165 170 175

aag aaa ggg ggt att ttc tcc gca gaa ttt ctg aag gtg ttc att cca 697
Lys Lys Gly Gly Ile Phe Ser Ala Glu Phe Leu Lys Val Phe Ile Pro
180 185 190

tct ctc ttc ctt tct cat gtt ttg gct ttg ggg cta ggc atc tat att 745
Ser Leu Phe Leu Ser His Val Leu Ala Leu Gly Leu Gly Ile Tyr Ile
195 200 205

gga aag cga ctg agc aca ccc tct gcc agc acc tac tga gggaaaggaa 794
Gly Lys Arg Leu Ser Thr Pro Ser Ala Ser Thr Tyr *
210 215

aagcccctgg aaatgcgtgt gacctgtgaa gtgggtgtatt gtcacagtag cttattttgaa 854
cttgagacca ttgtaagcat gacccaacct accaccctgt ttttacatat ccaattccag 914
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seq1ist.txt

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1 5 10 15	
atc agt gat gaa cat ggc atc gac ccc acc ggc acc tac cac ggg gac	96
Ile Ser Asp Glu His Gly Ile Asp Pro Thr Gly Thr Tyr His Gly Asp	
20 25 30	
agc gac ctg cag ctg gac cgc atc tct gtg tac tac aat gaa gcc aca	144
Ser Asp Leu Gln Leu Asp Arg Ile Ser Val Tyr Tyr Asn Glu Ala Thr	
35 40 45	
ggt ggc aaa tat gtt cct cgt gcc atc ctg gtg gat cta gaa cct ggg	192
Gly Gly Lys Tyr Val Pro Arg Ala Ile Leu Val Asp Leu Glu Pro Gly	
50 55 60	
acc atg gac tct gtt cgc tca ggt cct ttt ggc cag atc ttt aga cca	240
Thr Met Asp Ser Val Arg Ser Gly Pro Phe Gly Gln Ile Phe Arg Pro	

seq1ist.txt																
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ggc Gly	cac His	tac Tyr	aca Thr 100	gag Glu	ggc Gly	gcc Ala	gag Glu	ctg Leu 105	gtt Val	gat Asp	tct Ser	gtc Val	ctg Leu 110	gat Asp	gtg Val	336
gta Val	cgg Arg	aag Lys 115	gag Glu	gca Ala	gag Glu	agc Ser	tgt Cys 120	gac Asp	tgc Cys	ctg Leu	cag Gln	ggc Gly 125	ttc Phe	cag Gln	ctg Leu	384
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atc Ile 145	agc Ser	aag Lys	atc Ile	cga Arg	gaa Glu 150	gaa Glu	tac Tyr	cct Pro	gat Asp	cgc Arg 155	atc Ile	atg Met	aat Asn	acc Thr	ttc Phe 160	480
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aat Asn	gcc Ala	acc Thr	ctc Leu 180	tcc Ser	gtc Val	cat His	cag Gln	ttg Leu 185	gta Val	gag Glu	aat Asn	act Thr	gat Asp 190	gag Glu	acc Thr	576
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agg Arg	ctg Leu 210	acc Thr	aca Thr	cca Pro	acc Thr	tac Tyr 215	ggg Gly	gat Asp	ctg Leu	aac Asn	cac His 220	ctt Leu	gtc Val	tca Ser	ggc Gly	672
acc Thr 225	atg Met	gag Glu	tgt Cys	gtc Val	acc Thr 230	acc Thr	tgc Cys	ctc Leu	cgt Arg	ttc Phe 235	cct Pro	ggc Gly	cag Gln	ctc Leu	aat Asn 240	720
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gcc Ala	aag Lys 290	aac Asn	atg Met	atg Met	gct Ala	gcc Ala 295	tgt Cys	gac Asp	ccc Pro	cgc Arg	cac His 300	ggc Gly	cga Arg	tac Tyr	ctc Leu	912
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gag Glu	cag Gln	atg Met	ctt Leu	aac Asn 325	gtg Val	cag Gln	aac Asn	aag Lys	aac Asn 330	agc Ser	agc Ser	tac Tyr	ttt Phe	gtg Val 335	gaa Glu	1008
tgg Trp	atc Ile	ccc Pro	aac Asn	aat Asn	gtc Val	aag Lys	aca Thr	gcc Ala	gtc Val	tgt Cys	gac Asp	atc Ile	cca Pro	cct Pro	cgt Arg	1056

seqlist.txt

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Lys Ala Phe Leu His Trp Tyr Thr Gly Glu Gly Met Asp Glu Met Glu			
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Phe Thr Glu Ala Glu Ser Asn Met Asn Asp Leu Val Ser Glu Tyr Gln			
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Gln Tyr Gln Asp Ala Thr Ala Glu Glu Glu Glu Asp Phe Gly Glu Glu			
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Ala Glu Glu Glu Ala *			
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seq1ist.txt

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ctc cta aaa cac ctg gaa ggt atc tca gat gaa gac atc atc aac att Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile Asn Ile 195 200 205 210			740
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cgt gct gtt ggg cct cat cag ttc ctg ggt gac caa gag gcg atc caa Arg Ala Val Gly Pro His Gln Phe Leu Gly Asp Gln Glu Ala Ile Gln 230 235 240			836
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aaa tag tctttctcaa ctgttggcta agaagaaatg caaaagaagt ggcataggag Lys *			940
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seqlist.txt

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mRNA coding region

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Thr Ser Leu Leu Gly Lys Val Val Lys Thr His Gln Phe Leu Phe Gly
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Phe Lys Thr Asp Leu Pro Ser Ser Leu Val Ser Val Ser Leu Arg Lys
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Cys Ser Asn Asp Tyr Leu Gly Met Ser Arg His Pro Gln Val Leu Gln
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Ala Thr Gln Glu Thr Leu Gln Arg His Gly Ala Gly Ala Gly Gly Thr
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      220
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seq1ist.txt																
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ggg Gly 275	tgc Cys	gag Glu	att Ile	tac Tyr	tca Ser 280	gac Asp	gca Ala	ggc Gly	aac Asn	cat His 285	gct Ala	tcc Ser	atg Met	atc Ile	caa Gln 290	922
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ccc Pro	ctc Leu 340	gag Glu	gag Glu	ttg Leu	tgt Cys	gat Asp 345	gtg Val	tcc Ser	cac His	cag Gln	tat Tyr 350	ggg Gly	gcc Ala	ctg Leu	acc Thr	1114
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seq1ist.txt

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seq1ist.txt																
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seq1ist.txt

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Gln	Glu	Glu	Tyr	Glu	Asp	Pro	Asp	Ile	Pro	Glu	Ser	Gln	Met	Glu	Glu	
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Pro	Ala	Ala	His	Asp	Thr	Glu	Ala	Thr	Ala	Thr	Asp	Tyr	His	Thr	Thr	
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Met	Asp	Glu	Lys	Asn	Gln	Glu	Leu	Arg	Trp	Met	Glu	Ala	Ala	Arg	Trp	
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ttc Phe	acc Thr 115	aag Lys	ggt Gly	act Thr	gtt Val	ctc Leu 120	cta Leu	gac Asp	ctg Leu	caa Gln	gag Glu 125	acc Thr	tcc Ser	ctg Leu	gct Ala	501
gga Gly 130	gtg Val	gcc Ala	aac Asn	caa Gln	ctg Leu 135	cta Leu	gac Asp	agg Arg	ttt Phe	atc Ile 140	ttt Phe	gaa Glu	gac Asp	cag Gln	atc Ile 145	549
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ggg Gly 210	cac His	tca Ser	cca Pro	tct Ser	gga Gly 215	att Ile	ctg Leu	gaa Glu	aag Lys	att Ile 220	ccc Pro	ccg Pro	gat Asp	tca Ser	gag Glu 225	789
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cct Pro	ccc Pro	acc Thr	gat Asp 325	gcc Ala	ccc Pro	tcc Ser	gag Glu	cag Gln 330	gca Ala	ctg Leu	ctc Leu	agt Ser	ctg Leu 335	gtg Val	cct Pro	1125
gtg Val	cag Gln	agg Arg 340	gag Glu	cta Leu	ctt Leu	cga Arg	agg Arg 345	cgc Arg	tat Tyr	cag Gln	tcc Ser	agc Ser 350	cct Pro	gcc Ala	aag Lys	1173
cca Pro	gac Asp	tcc Ser	agc Ser	ttc Phe	tac Tyr	aag Lys	ggc Gly	cta Leu	gac Asp	tta Leu	aat Asn	ggg Gly	ggc Gly	cca Pro	gat Asp	1221

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atc Ile	cgg Arg	cgc Arg	cgc Arg	tac Tyr 390	ccc Pro	tat Tyr	tac Tyr	ctg Leu	agt Ser 395	gac Asp	atc Ile	aca Thr	gat Asp	gca Ala 400	ttc Phe		1317
agc Ser	ccc Pro	cag Gln	gtc Val 405	ctg Leu	gct Ala	gcc Ala	gtc Val	atc Ile 410	ttc Phe	atc Ile	tac Tyr	ttt Phe	gct Ala 415	gca Ala	ctg Leu		1365
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Gly Ser Thr Glu Asp Gly Asp Gly Thr Asp Asp Phe Leu Thr Asp Lys	
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Cys Gln Trp Leu Pro Ile Leu Ile Leu Leu Gly Thr Gly His Gly	
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Pro Gly Val Glu Gly Val Thr His Tyr Lys Ala Gly Asp Pro Val Ile	
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Met	Phe	Asn	Val	His	Arg	His	Gly	Ala	Ile	Asn	Ser	Ala	Ala	Ile	Leu			
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seqlist.txt

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 gcctccgaca gcgctccgga gggaccgggg gagctcccag gcgcccggga ctggagactg 240
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 Met Thr Val Phe Arg Gln
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 gac ttc tta gct gaa aag gaa tct tta act gaa gag gaa gca act gaa 690
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seq1ist.txt

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gca tca gac ctg aac ctc ctc act cgg agg aaa ctg agt cgc ctg ctg 4290
Ala Ser Asp Leu Asn Leu Leu Thr Arg Arg Lys Leu Ser Arg Leu Leu
1305 1310 1315

gac ccg ccc gac ccc ctg ggg aag gac tgg tgc ctt ctc gcc atg aac 4338
Asp Pro Pro Asp Pro Leu Gly Lys Asp Trp Cys Leu Leu Ala Met Asn
1320 1325 1330

tta ggc ctc cct gac ctc gtg gca aag tac aac acc aat aac ggg gct 4386
Leu Gly Leu Pro Asp Leu Val Ala Lys Tyr Asn Thr Asn Asn Gly Ala
1335 1340 1345 1350

ccc aag gat ttc ctc ccc agc ccc ctc cac gcc ctg ctg cgg gaa tgg 4434
Pro Lys Asp Phe Leu Pro Ser Pro Leu His Ala Leu Leu Arg Glu Trp
1355 1360 1365

acc acc tac cct gag agc aca gtg ggc acc ctc atg tcc aaa ctg agg 4482
Thr Thr Tyr Pro Glu Ser Thr Val Gly Thr Leu Met Ser Lys Leu Arg
1370 1375 1380

gag ctg ggt cgc cgg gat gcc gca gac ctt ttg ctg aag gca tcc tct 4530
Glu Leu Gly Arg Arg Asp Ala Ala Asp Leu Leu Leu Lys Ala Ser Ser
1385 1390 1395

gtg ttc aaa atc aac ctg gat ggc aat ggc cag gag gcc tat gcc tcg 4578
Val Phe Lys Ile Asn Leu Asp Gly Asn Gly Gln Glu Ala Tyr Ala Ser
1400 1405 1410

agc tgc aac agc ggc acc tct tac aat tcc att agc tct gtt gta tcc 4626
Ser Cys Asn Ser Gly Thr Ser Tyr Asn Ser Ile Ser Ser Val Val Ser
1415 1420 1425 1430

cgg tga gggcagcctc tggcttggac agggctctgtt tggactgcag aaccaagggg 4682
Arg *

```

```

gtgatgtagc ccattccttcc ctttggagat gctgaggggtg tttcttccctg caccacagc 4742
caggggggatg ccactcctcc ctccggcttg acctgtttct ctgccgctac ctccctcccc 4802
gtctcattcc gttgtctgtg gatggtcatt gcagtttaag agcagaacag atcttttact 4862
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ccagtacctt gcttcttact gataattttg ctggaattcc taacttttca atgacatttt 4982
ttttaactat catattgatt gtccttttaa aaagaaaagt gcatattttat ccaaaatgtg 5042
tatttcttat acgcttttct gtgttatacc atttcctcag cttatctctt ttatatattgt 5102
aggagaaact cccatgtatg gaatcccact gtatgattta taaacagaca atatgtgagt 5162
gcctttttgca gaagaggggtg tgtttgaaat catcggagtc agccaggagc tgtcaccaag 5222
gaaacgctac ctctctgtcc cttgctgtat gctgatcatc gccagaggtg cttcaccctg 5282
agttttgttt tgtattgttt tctgacagtt tttctgtttt gtttggcaag gaaaggggag 5342
aagggaatcc tcctccaggg tgattttatg atcagtgttg ttgctctagg aagacatttt 5402
tccgtttgct tttgttccaa tgtcaatgtg aacgtccaca tgaaacctac acactgtcat 5462
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tatatcatat gtatatatat atatgcacta tgtatataca tatatattaa tactgggtatt 5822
tttacttaat ctataaaatg tcgttaaaaaa gttgtttgtt tttttctttt tttataaata 5882
aactgttgct cgttaaaaaa aaaaaaaa 5910

```

```

<210> 12
<211> 1579
<212> DNA
<213> Homo sapiens

```

seqlist.txt

<220>

<221> CDS

<222> (313)...(867)

<223> Human RAP1A, member of RAS oncogene family (RAP1A)
mRNA coding region

<400> 12

```

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ctgccgggttc gaacacacgc gagaagagca aagaagttaa aagagaagtg tctgtgtggc 120
tcctttccacg tgggtgaagg actgtgccag ctgagaggtg gtagagcagg aagctgcctg 180
agacctccat ttatttggtg aaaaaccgcc gcccttaaga gagcaagtcg agggccgtgt 240
aggagttgga ggagagaaat gaaatttttg aagagtcagc agaagatcgt cagtatttaa 300
acacatcaca tc atg cgt gag tac aag cta gtg gtc ctt ggt tca gga ggc 351
          Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly
                1             5             10

```

```

gtt ggg aag tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt 399
Val Gly Lys Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val
          15             20             25

```

```

gaa aaa tat gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa 447
Glu Lys Tyr Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu
          30             35             40             45

```

```

gtc gat tgc caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca 495
Val Asp Cys Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr
          50             55             60

```

```

gag caa ttt aca gca atg agg gat ttg tat atg aag aac ggc caa ggt 543
Glu Gln Phe Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly
          65             70             75

```

```

ttt gca cta gta tat tct att aca gct cag tcc acg ttt aac gac tta 591
Phe Ala Leu Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu
          80             85             90

```

```

cag gac ctg agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt 639
Gln Asp Leu Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val
          95             100             105

```

```

cca atg att ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta 687
Pro Met Ile Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val
          110             115             120             125

```

```

gtt ggc aaa gag cag ggc cag aat tta gca aga cag tgg tgt aac tgt 735
Val Gly Lys Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys
          130             135             140

```

```

gcc ttt tta gaa tct tct gca aag tca aag atc aat gtt aat gag ata 783
Ala Phe Leu Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile
          145             150             155

```

```

ttt tat gac ctg gtc aga cag ata aat agg aaa aca cca gtg gaa aag 831
Phe Tyr Asp Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys
          160             165             170

```

```

aag aag cct aaa aag aaa tca tgt ctg ctg ctc tag gcccatagtc 877
Lys Lys Pro Lys Lys Lys Ser Cys Leu Leu Leu *
          175             180

```

```

agcagcagct ctgagccaga ttacaggaat gaagaactgt tgcctaattg gaaagtgcc 937
gcattccaga cttcaaaaat aaaaaatctg aagaggcttc tcctgtttta tatattatgt 997
gaagaattta gatcttatat tggtttgcac aagttccctg gagaaaaaaa ttgctctgtg 1057
tatatctctt ggaaaataag acaatagtat ttctcctttg caatagcagt tataacagat 1117
gtgaaaatat acttgactct aatatgatta tacaaaagag catggatgca tttcaaatgt 1177
tagatattgc tactataatc aaatgatttc atattgatct ttttatcatg atcctaccta 1237
tcaagcacta aaaagttgaa ccattatact ttatatctgt aatgatactg attatgaaat 1297
gtcccctgaa actcattgca gcagataact tttttgagtc attgacttca ttttatattt 1357

```


seq1ist.txt

```

aaaaaattat ggaatatcat ctgtcattat attctaatta aaattgtgca taatgctttg 1417
gaaaaatggg tcttttatag gaaaaaaaact gggataactg atttctatgg ctttcaaagc 1477
taaaatatat aatatactaa accaactcta atattgcttc ttgtgtttta ctgtcagatt 1537
aaattacagc ttttatggat gattaaattt tagtacattt tc 1579

```

```

<210> 13
<211> 3222
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> CDS
<222> (0)...(0)
<223> Human down-regulator of transcription 1,
      TBP-binding (negative cofactor 2) (DR1) mRNA
      coding region

```

```

<400> 13
gagcggcttc ctgcaaacct tccctggcat ctggaggggac caccgttgcc gcgtcttcgg 60
cttccacgat ctgcgttcgg gctacgcggc cacggcggca gccactgcga ctcccactgt 120
gcctggctct gtccatatta gttcccaggc ggccgtcggc gttccagcag cggcagcggc 180
agcggcagcg gcggacatgt tgtgaggcgg cggcgcgggt gtctgaagga tggtttgggc 240
gaggcggcgg caacggctgc tggcggcggc ggagcggcga gcggggcctc gggctctata 300
gagccgagcc cgctgggtac ccgcccggta ccgcggcgag gccagtggcc ctggatcttg 360
cctctgctcc gacgccgttg gggaccagtt aggcgacagc gcccgcccct ctgaggagac 420
acgaagggtg ttccccagcc gctcaaattt ccggaccacc gcgctttccc ctctcagacc 480
tgggctgtgc tctctctaga atcctcgggc ccccactttc ttcccaaact catcctaaat 540
ctctcacaca cgcgagtgtt cccagccctc aagccagctg ctctccgagg cattttctgc 600
accctcttcg caaagcacc cccgggatca ctctccgagg gcgacttttt gagaaatctc 660
ggtggagtag tggaccagag ctggggagtt tttaaaagcc ggggcgcgag aacaggaag 720
gtactatggc ttctctgtct ggcaacgatg atgatctcac tatccccaga gctgctatca 780
ataaaatgat caaagagact cttcctaata tccgggtggc caacgatgct cgagagctgg 840
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acaaatcgga aaagaagacc atctcaccag agcatgtcat acaagcacta gaaagtgttg 960
gattttggctc ttacatcagt gaagtaaaag aagtcttgca agagtgtaaa acagtagcat 1020
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ttaattttgc tgaatgtttt aagttgaagt tacttcatgg atgtcatacc catgaagtgc 2880
atttgatga gatagaagaa attgtttttt aaaaagttaa agtaccaaag gtagtctagt 2940
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```

seq1ist.txt

```

ttctattttta agtataatctg tttctttaagt aaacaactta gatatttttcc acacctttttt 3060
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tttgaagcct agtgactttt catttttgaca ttcttgatgat ttcataatgct gtattcttca 3180
agcaataaaa ttgtgatgtg ttttataaaa aaaaaaaaaa aa 3222

```

<210> 14
 <211> 3541
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (76)...(3504)
 <223> Human Janus kinase 1 (JAK1) mRNA coding region

<400> 14
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 gaggactgca atgcc atg gct ttc tgt gct aaa atg agg agc tcc aag aag 111
 Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys
 1 5 10

act gag gtg aac ctg gag gcc cct gag cca ggg gtg gaa gtg atc ttc 159
 Thr Glu Val Asn Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe
 15 20 25

tat ctg tcg gac agg gag ccc ctc cgg ctg ggc agt gga gag tac aca 207
 Tyr Leu Ser Asp Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr
 30 35 40

gca gag gaa ctg tgc atc agg gct gca cag gca tgc cgt atc tct cct 255
 Ala Glu Glu Leu Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro
 45 50 55 60

ctt tgt cac aac ctc ttt gcc ctg tat gac gag aac acc aag ctc tgg 303
 Leu Cys His Asn Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp
 65 70 75

tat gct cca aat cgc acc atc acc gtt gat gac aag atg tcc ctc cgg 351
 Tyr Ala Pro Asn Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg
 80 85 90

ctc cac tac cgg atg agg ttc tat ttc acc aat tgg cat gga acc aac 399
 Leu His Tyr Arg Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn
 95 100 105

gac aat gag cag tca gtg tgg cgt cat tct cca aag aag cag aaa aat 447
 Asp Asn Glu Gln Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn
 110 115 120

ggc tac gag aaa aaa aag att cca gat gca acc cct ctc ctt gat gcc 495
 Gly Tyr Glu Lys Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala
 125 130 135 140

agc tca ctg gag tat ctg ttt gct cag gga cag tat gat ttg gtg aaa 543
 Ser Ser Leu Glu Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys
 145 150 155

tgc ctg gct cct att cga gac ccc aag acc gag cag gat gga cat gat 591
 Cys Leu Ala Pro Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp
 160 165 170

att gag aac gag tgt cta ggg atg gct gtc ctg gcc atc tca cac tat 639
 Ile Glu Asn Glu Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr
 175 180 185

gcc atg atg aag aag atg cag ttg cca gaa ctg ccc aag gac atc agc 687
 Ala Met Met Lys Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser
 190 195 200

seqlist.txt

tac Tyr 205	aag Lys	cga Arg	tat Tyr	att Ile	cca Pro 210	gaa Glu	aca Thr	ttg Leu	aat Asn	aag Lys 215	tcc Ser	atc Ile	aga Arg	cag Gln	agg Arg 220	735
aac Asn	ctt Leu	ctc Leu	acc Thr	agg Arg 225	atg Met	cgg Arg	ata Ile	aat Asn	aat Asn 230	gtt Val	ttc Phe	aag Lys	gat Asp	ttc Phe 235	cta Leu	783
aag Lys	gaa Glu	ttt Phe	aac Asn 240	aac Asn	aag Lys	acc Thr	att Ile	tgt Cys 245	gac Asp	agc Ser	agc Ser	gtg Val	tcc Ser 250	acg Thr	cat His	831
gac Asp	ctg Leu	aag Lys 255	gtg Val	aaa Lys	tac Tyr	ttg Leu	gct Ala 260	acc Thr	ttg Leu	gaa Glu	act Thr	ttg Leu 265	aca Thr	aaa Lys	cat His	879
tac Tyr	ggt Gly 270	gct Ala	gaa Glu	ata Ile	ttt Phe	gag Glu 275	act Thr	tcc Ser	atg Met	tta Leu	ctg Leu 280	att Ile	tca Ser	tca Ser	gaa Glu	927
aat Asn 285	gag Glu	atg Met	aat Asn	tgg Trp	ttt Phe 290	cat His	tcg Ser	aat Asn	gac Asp	ggt Gly 295	gga Gly	aac Asn	gtt Val	ctc Leu	tac Tyr 300	975
tac Tyr	gaa Glu	gtg Val	atg Met	gtg Val 305	act Thr	ggg Gly	aat Asn	ctt Leu	gga Gly 310	atc Ile	cag Gln	tgg Trp	agg Arg	cat His 315	aaa Lys	1023
cca Pro	aat Asn	gtt Val	gtt Val 320	tct Ser	gtt Val	gaa Glu	aag Lys	gaa Glu 325	aaa Lys	aat Asn	aaa Lys	ctg Leu	aag Lys 330	cgg Arg	aaa Lys	1071
aaa Lys	ctg Leu	gaa Glu 335	aat Asn	aaa Lys	gac Asp	aag Lys	aag Lys 340	gat Asp	gag Glu	gag Glu	aaa Lys	aac Asn 345	aag Lys	atc Ile	cgg Arg	1119
gaa Glu	gag Glu 350	tgg Trp	aac Asn	aat Asn	ttt Phe	tca Ser 355	ttc Phe	ttc Phe	cct Pro	gaa Glu	atc Ile 360	act Thr	cac His	att Ile	gta Val	1167
ata Ile 365	aag Lys	gag Glu	tct Ser	gtg Val	gtc Val 370	agc Ser	att Ile	aac Asn	aag Lys	cag Gln 375	gac Asp	aac Asn	aag Lys	aaa Lys	atg Met 380	1215
gaa Glu	ctg Leu	aag Lys	ctc Leu	tct Ser 385	tcc Ser	cac His	gag Glu	gag Glu	gcc Ala 390	ttg Leu	tcc Ser	ttt Phe	gtg Val	tcc Ser 395	ctg Leu	1263
gta Val	gat Asp	ggc Gly	tac Tyr 400	ttc Phe	cgg Arg	ctc Leu	aca Thr	gca Ala 405	gat Asp	gcc Ala	cat His	cat His	tac Tyr 410	ctc Leu	tgc Cys	1311
acc Thr	gac Asp	gtg Val 415	gcc Ala	ccc Pro	ccg Pro	ttg Leu	atc Ile 420	gtc Val	cac His	aac Asn	ata Ile	cag Gln 425	aat Asn	ggc Gly	tgt Cys	1359
cat His	ggt Gly 430	cca Pro	atc Ile	tgt Cys	aca Thr	gaa Glu 435	tac Tyr	gcc Ala	atc Ile	aat Asn	aaa Lys 440	ttg Leu	cgg Arg	caa Gln	gaa Glu	1407
gga Gly 445	agc Ser	gag Glu	gag Glu	ggg Gly 450	atg Met	tac Tyr	gtg Val	ctg Leu	agg Arg	tgg Trp 455	agc Ser	tgc Cys	acc Thr	gac Asp	ttt Phe 460	1455
gac Asp	aac Asn	atc Ile	ctc Leu	atg Met 465	acc Thr	gtc Val	acc Thr	tgc Cys	ttt Phe 470	gag Glu	aag Lys	tct Ser	gag Glu	cag Gln 475	gtg Val	1503

seq1ist.txt

cag Gln	ggt Gly	gcc Ala	cag Gln 480	aag Lys	cag Gln	ttc Phe	aag Lys	aac Asn 485	ttt Phe	cag Gln	atc Ile	gag Glu	gtg Val 490	cag Gln	aag Lys	1551
ggc Gly	cgc Arg	tac Tyr 495	agt Ser	ctg Leu	cac His	ggt Gly	tcg Ser 500	gac Asp	cgc Arg	agc Ser	ttc Phe	ccc Pro 505	agc Ser	ttg Leu	gga Gly	1599
gac Asp	ctc Leu 510	atg Met	agc Ser	cac His	ctc Leu	aag Lys 515	aag Lys	cag Gln	atc Ile	ctg Leu	cgc Arg 520	acg Thr	gat Asp	aac Asn	atc Ile	1647
agc Ser 525	ttc Phe	atg Met	cta Leu	aaa Lys	cgc Arg 530	tgc Cys	tgc Cys	cag Gln	ccc Pro	aag Lys 535	ccc Pro	cga Arg	gaa Glu	atc Ile	tcc Ser 540	1695
aac Asn	ctg Leu	ctg Leu	gtg Val 545	gct Ala	act Thr	aag Lys	aaa Lys	gcc Ala	cag Gln 550	gag Glu	tgg Trp	cag Gln	ccc Pro	gtc Val 555	tac Tyr	1743
ccc Pro	atg Met	agc Ser	cag Gln 560	ctg Leu	agt Ser	ttc Phe	gat Asp	cgg Arg 565	atc Ile	ctc Leu	aag Lys	aag Lys	gat Asp 570	ctg Leu	gtg Val	1791
cag Gln	ggc Gly	gag Glu 575	cac His	ctt Leu	ggg Gly	aga Arg	ggc Gly 580	acg Thr	aga Arg	aca Thr	cac His	atc Ile 585	tat Tyr	tct Ser	ggg Gly	1839
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ata Ile 605	aaa Lys	gtg Val	atc Ile	ctc Leu	aaa Lys 610	gtc Val	tta Leu	gac Asp	ccc Pro	agc Ser 615	cac His	agg Arg	gat Asp	att Ile	tcc Ser 620	1935
ctg Leu	gcc Ala	ttc Phe	ttc Phe	gag Glu 625	gca Ala	gcc Ala	agc Ser	atg Met	atg Met 630	aga Arg	cag Gln	gtc Val	tcc Ser	cac His 635	aaa Lys	1983
cac His	atc Ile	gtg Val	tac Tyr 640	ctc Leu	tat Tyr	ggc Gly	gtc Val	tgt Cys 645	gtc Val	cgc Arg	gac Asp	gtg Val	gag Glu 650	aat Asn	atc Ile	2031
atg Met	gtg Val	gaa Glu 655	gag Glu	ttt Phe	gtg Val	gaa Glu	ggg Gly 660	ggt Gly	cct Pro	ctg Leu	gat Asp	ctc Leu 665	ttc Phe	atg Met	cac His	2079
cgg Arg	aaa Lys 670	agt Ser	gat Asp	gtc Val	ctt Leu	acc Thr 675	aca Thr	cca Pro	tgg Trp	aaa Lys	ttc Phe 680	aaa Lys	gtt Val	gcc Ala	aaa Lys	2127
cag Gln 685	ctg Leu	gcc Ala	agt Ser	gcc Ala	ctg Leu 690	agc Ser	tac Tyr	ttg Leu	gag Glu	gat Asp 695	aaa Lys	gac Asp	ctg Leu	gtc Val	cat His 700	2175
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agt Ser	gag Glu	tgt Cys	ggc Gly 720	cca Pro	ttc Phe	atc Ile	aag Lys	ctc Leu 725	agt Ser	gac Asp	ccc Pro	ggc Gly	atc Ile 730	ccc Pro	att Ile	2271
acg Thr	gtg Val	ctg Leu 735	tct Ser	agg Arg	caa Gln	gaa Glu	tgc Cys 740	att Ile	gaa Glu	cga Arg	atc Ile	cca Pro 745	tgg Trp	att Ile	gct Ala	2319

seqlist.txt

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765					770					775					780	
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seqlist.txt

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Ala Pro Glu Cys Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val
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tgg tct ttt gga gtc act ctg cat gag ctg ctg act tac tgt gat tca 3279
Trp Ser Phe Gly Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser
1055 1060 1065

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Gly Gln Met Thr Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys
1085 1090 1095 1100

cgc ctg ccg tgc cca cct aac tgt cca gat gag gtt tat cag ctt atg 3423
Arg Leu Pro Cys Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met
1105 1110 1115

aga aaa tgc tgg gaa ttc caa cca tcc aat cgg aca agc ttt cag aac 3471
Arg Lys Cys Trp Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn
1120 1125 1130

ctt att gaa gga ttt gaa gca ctt tta aaa taa gaagcatgaa taacatttaa 3524
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Met Arg Glu Cys Ile Ser Ile His Val Gly Gln Ala Gly Val
1 5 10

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Gln Ile Gly Asn Ala Cys Trp Glu Leu Tyr Cys Leu Glu His Gly Ile
15 20 25 30

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Gln Pro Asp Gly Gln Met Pro Ser Asp Lys Thr Ile Gly Gly Gly Asp
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gac tcc ttc aac acc ttc ttc agt gag acg ggc gct ggc aag cac gtg 253
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Gly	Lys	Glu	Asp	Ala	Ala	Asn	Asn	Tyr	Ala	Arg	Gly	His	Tyr	Thr	Ile	
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Gly	Gly	Thr	Gly	Ser	Gly	Phe	Thr	Ser	Leu	Leu	Met	Glu	Arg	Leu	Ser	
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Val	Asp	Tyr	Gly	Lys	Lys	Ser	Lys	Leu	Glu	Phe	Ser	Ile	Tyr	Pro	Ala	
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Pro	Gln	Val	Ser	Thr	Ala	Val	Val	Glu	Pro	Tyr	Asn	Ser	Ile	Leu	Thr	
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Glu	Ala	Ile	Tyr	Asp	Ile	Cys	Arg	Arg	Asn	Leu	Asp	Ile	Glu	Arg	Pro	
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Thr	Tyr	Thr	Asn	Leu	Asn	Arg	Leu	Ile	Ser	Gln	Ile	Val	Ser	Ser	Ile	
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act	gct	tcc	ctg	aga	ttt	gat	gga	gcc	ctg	aat	gtt	gac	ctg	aca	gaa	829
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Tyr	Arg	Gly	Asp	Val	Val	Pro	Lys	Asp	Val	Asn	Ala	Ala	Ile	Ala	Thr	
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Ile	Lys	Thr	Lys	Arg	Thr	Ile	Gln	Phe	Val	Asp	Trp	Cys	Pro	Thr	Gly	
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seqlist.txt

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gcc att gct gag gcc tgg gct cgc ctg gac cac aag ttt gac ctg atg	1261
Ala Ile Ala Glu Ala Trp Ala Arg Leu Asp His Lys Phe Asp Leu Met	
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tat gcc aag cgt gcc ttt gtt cac tgg tac gtg ggt gag ggg atg gag	1309
Tyr Ala Lys Arg Ala Phe Val His Trp Tyr Val Gly Glu Gly Met Glu	
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Gly Ser Ser Gly Pro Trp Ser Leu Ser Pro Ser Asp Ser Ser Pro Ser	
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Gly Val Thr Ser Arg Leu Pro Gly Arg Ser Thr Ser Leu Val Glu Gly	
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cgc agc tgt ggc tgg gtg ccc cca ccc cct ggc ttc gca ccg ctg gct	299
Arg Ser Cys Gly Trp Val Pro Pro Pro Pro Gly Phe Ala Pro Leu Ala	
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ccc cgc ctg ggc cct gag ctg tca ccc tca ccc act tcg ccc act gca	347
Pro Arg Leu Gly Pro Glu Leu Ser Pro Ser Pro Thr Ser Pro Thr Ala	
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seqlist.txt

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Leu Pro Leu Ser Pro Ser Ala Phe Ser Ala Ala Pro Gly Thr Pro Leu
225 230 235 240

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Ala Arg Arg Asp Pro Thr Pro Val Cys Cys Pro Ser Cys Arg Arg Ala
245 250 255

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Arg Ile Ser Val Ser Glu *
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6p12.1-21.1; accession number AL031778

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kinase kinase 2 (MAP4K2) mRNA coding region

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cgcccgctg ccggcccgcc cggcgcccgg cc atg gcg ctg ctg cgg gat gtg 113
Met Ala Leu Leu Arg Asp Val
1 5

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Ser Leu Gln Asp Pro Arg Asp Arg Phe Glu Leu Leu Gln Arg Val Gly
10 15 20

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25 30 35

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